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TECH CENTER 1600/2900

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TECH CENTER 1600/2900

Sequence Listing

<110> Adams, Sean
Pan, James
Zhong, Alan

<120> UCP4

<130> P1626R1

<140> US 09/397,342

<141> 1999-09-15

<150> US 60/101,279

<151> 1998-09-22

<150> US 60/114,223

<151> 1998-12-30

<150> US 60/129,674

<151> 1999-04-16

<160> 18

<210> 1

<211> 323

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
65 70 75

Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
125 130 135

Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	
				305					310					315	
Glu	Met	Ser	Gly	Val	Ser	Pro	Phe								
				320											

<210> 2
 <211> 1039
 <212> DNA
 <213> Homo sapiens

<400> 2
 ccgagctcgg atcccgttat cgtcttgccg tactgctgaa tgtccgtccc 50
 ggaggaggag gagaggcttt tgccgctgac ccagagatgg ccccgagcga 100
 gcaaattcct actgtccggc tgcgcggcta ccgtggccga gctagcaacc 150
 tttcccctgg atctcacaaa aactcgactc caaatgcaag gagaagcagc 200
 tcttgctcgg ttgggagacg gtgcaagaga atctgcccc tataggggaa 250
 tggtgccgac agccctaggg atcattgaag aggaaggctt tctaaagctt 300
 tggcaaggag tgacacccgc catttacaga cacgtagtgt attctggagg 350

tcgaatggtc acatatgaac atctccgaga gggtgtgttt ggcaaaagtg 400
 aagatgagca ttatcccctt tggaaatcag tcattggagg gatgatggct 450
 ggtgttattg gccagttttt agccaatcca actgacctag tgaaggttca 500
 gatgcaaatg gaaggaaaaa ggaaactgga aggaaaacca ttgcgatttc 550
 gtggtgtaca tcatgcattt gcaaaaatct tagctgaagg aggaatacga 600
 gggcttttggg caggctgggt acccaatata caaagagcag cactggtgaa 650
 tatgggagat ttaaccactt atgatacagt gaaacactac ttggtattga 700
 atacaccact tgaggacaat atcatgactc acggtttata aagtttatgt 750
 tctggactgg tagcttctat tctgggaaca ccagccgatg tcatcaaaag 800
 cagaataatg aatcaaccac gagataaaca aggaagggga cttttgtata 850
 aatcatcgac tgactgcttg attcaggctg ttcaaggtga aggattcatg 900
 agtctatata aaggcttttt accatcttgg ctgagaatga ccccttggtc 950
 aatggtgttc tggcttactt atgaaaaaat cagagagatg agtggagtca 1000
 gtccatttta agaattctgc agatatccat cacactggc 1039

<210> 3
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <221> Misc-feature
 <222> 1-31
 <223> Sequence is synthesized

<400> 3
 cgcgatccc gttatcgtct tgcgctactg c 31

<210> 4
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <221> Misc-feature
 <222> 1-34
 <223> Sequence is synthesized

<400> 4
 gcggaattct taaaatggac tgactccact catc 34

<210> 5
 <211> 1248
 <212> DNA
 <213> Artificial

<220>
<221> Misc-feature
<222> 1-1248
<223> Sequence is synthesized

<220>
<221> unsure
<222> 1231
<223> unknown base

<400> 5
cgttatcgtc ttgcgctact gctgaatgtc cgtcccggag gaggaggaga 50
ggcttttgcc gctgaccag agatggcccc gagcgagcaa attcctactg 100
tccggctgcg cggctaccgt ggccgagcta gcaacctttc ccctggatct 150
cacaaaaact cgactccaaa tgcaaggaga agcagctctt gctcggttgg 200
gagacggtgc aagagaatct gccccctata ggggaatggt gcgcacagcc 250
ctagggatca ttgaagagga aggctttcta aagctttggc aaggagtgc 300
accgcgcatc tacagacacg tagttatttc tggaggctga atggtcacat 350
atgaacatct ccgagagggt gtgtttggca aaagtgaaga tgagcattat 400
cccctttgga aatcagtcac tggaggggat atggctggtg ttattggcca 450
gttttttagc aatccaactg acctagtga ggttcagatg caaatggaag 500
gaaaaaggaa actggaagga aaaccattgc gatttcgtgg tgtacatcat 550
gcatttgcaa aaatcttagc tgaaggagga atacgaaggc tttgggcagg 600
ctgggtaccc aatatacaaa gagcagcact ggtgaatatg ggagatttaa 650
ccacttatga tacagtgaac cactacttgg tattgaatac accacttgag 700
gacaatatca tgactcacgg tttatcaagt ttatgttctg gactggtagc 750
ttctattctg ggaacaccag ccgatgtcat caaaagcaga ataataatc 800
aaccacgaga taaacaagga aggggacttt tgtataaatc atcgactgac 850
tgcttgattc aggctgttca aggtgaagga ttcattgagc tatataaagg 900
ctttttacca tcttggtgga gaatgacccc ttggtcaatg gtgttctggc 950
ttacttatga aaaaatcaga gagatgagtg gagtcagtcc attttaaac 1000
cctaaagatg caacccttaa agatacagtg ttcagtatta ttgaaatatg 1050
ggcatctgca acacataccc cctattattt ctacctcttt aggaagacac 1100
ctattccaca gagactgatt tatagggggc agcactttat ttttttctgg 1150
aaaccaagt tctctttgac tcctcttttt gtccaaaagt gatctggtcg 1200

gatctcacaa ggccatccaa tgagaccccg nacagcattt tctaaaga 1248

<210> 6
<211> 58
<212> DNA
<213> Artificial

<220>
<221> Misc-feature
<222> 1-58
<223> Sequence is synthesized

<400> 6
cgcgatccg aaatggacta caaggacgac gatgacaagt ccgtcccga 50

ggaggagg 58

<210> 7
<211> 35
<212> DNA
<213> Artificial

<220>
<221> Misc-feature
<222> 1-35
<223> Sequence is synthesized

<400> 7
gcgaagcttg ccatggttg actgaagcct tcaga 35

<210> 8
<211> 33
<212> DNA
<213> Artificial

<220>
<221> Misc-feature
<222> 1-33
<223> Sequence is synthesized

<400> 8
cgcaattct caaaacggtg attcccgtta cat 33

<210> 9
<211> 61
<212> DNA
<213> Artificial

<220>
<221> Misc-feature
<222> 1-61
<223> Sequence is synthesized

<400> 9
gcgaagcttg ccatggacta caaggacgac gatgacaagg ttggactgaa 50

gccttcagac g 61

<210> 10
 <211> 19
 <212> DNA
 <213> Artificial

 <220>
 <221> Misc-feature
 <222> 1-19
 <223> Sequence is synthesized

 <400> 10
 aatgcctatc gccgaggag 19

 <210> 11
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Misc-feature
 <222> 1-20
 <223> Sequence is synthesized

 <400> 11
 gtaggaactt gctcgtccgg 20

 <210> 12
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Misc-feature
 <222> 1-22
 <223> Sequence is synthesized

 <400> 12
 tgctcgcgct cacgcagaga tg 22

 <210> 13
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Misc-feature
 <222> 1-24
 <223> Sequence is synthesized

 <400> 13
 gaaatcgtgc gtgacatcaa agag 24

 <210> 14
 <211> 23
 <212> DNA
 <213> Artificial

 <220>

<221> Misc-feature
<222> 1-23
<223> Sequence is synthesized

<400> 14
ctccttctgc atcctgtcag caa 23

<210> 15
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Misc-feature
<222> 1-22
<223> Sequence is synthesized

<400> 15
cggttccgat gccctgaggc tc 22

<210> 16
<211> 307
<212> PRT
<213> Homo sapiens

<400> 16
Met Gly Gly Leu Thr Ala Ser Asp Val His Pro Thr Leu Gly Val
1 5 10 15
Gln Leu Phe Ser Ala Pro Ile Ala Ala Cys Leu Ala Asp Val Ile
20 25 30
Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly
35 40 45
Glu Cys Pro Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly
50 55 60
Thr Ile Thr Ala Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr
65 70 75
Ser Gly Leu Pro Ala Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser
80 85 90
Leu Arg Ile Gly Leu Tyr Asp Thr Val Gln Glu Phe Leu Thr Ala
95 100 105
Gly Lys Glu Thr Ala Pro Ser Leu Gly Ser Lys Ile Leu Ala Gly
110 115 120
Leu Thr Thr Gly Gly Val Ala Val Phe Ile Gly Gln Pro Thr Glu
125 130 135
Val Val Lys Val Arg Leu Gln Ala Gln Ser His Leu His Gly Ile
140 145 150
Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala Tyr Arg Ile Ile Ala
155 160 165

Thr Thr Glu Gly	Leu Thr Gly Leu Trp	Lys Gly Thr Thr Pro	Asn
170		175	180
Leu Met Arg Ser	Val Ile Ile Asn Cys	Thr Glu Leu Val Thr	Tyr
185		190	195
Asp Leu Met Lys	Glu Ala Phe Val Lys	Asn Asn Ile Leu Ala	Asp
200		205	210
Asp Val Pro Cys	His Leu Val Ser Ala	Leu Ile Ala Gly Phe	Cys
215		220	225
Ala Thr Ala Met	Ser Ser Pro Val Asp	Val Val Lys Thr Arg	Phe
230		235	240
Ile Asn Ser Pro	Pro Gly Gln Tyr Lys	Ser Val Pro Asn Cys	Ala
245		250	255
Met Lys Val Phe	Thr Asn Glu Gly Pro	Thr Ala Phe Phe Lys	Gly
260		265	270
Leu Val Pro Ser	Phe Leu Arg Leu Gly	Ser Trp Asn Val Ile	Met
275		280	285
Phe Val Cys Phe	Glu Gln Leu Lys Arg	Glu Leu Ser Lys Ser	Arg
290		295	300
Gln Thr Met Asp	Cys Ala Thr		
305			

<210> 17
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 17

Met Val Gly Phe	Lys Ala Thr Asp Val	Pro Pro Thr Ala Thr	Val
1	5	10	15
Lys Phe Leu Gly	Ala Gly Thr Ala Ala	Cys Ile Ala Asp Leu	Ile
20		25	30
Thr Phe Pro Leu	Asp Thr Ala Lys Val	Arg Leu Gln Ile Gln	Gly
35		40	45
Glu Ser Gln Gly	Pro Val Arg Ala Thr	Val Ser Ala Gln Tyr	Arg
50		55	60
Gly Val Met Gly	Thr Ile Leu Thr Met	Val Arg Thr Glu Gly	Pro
65		70	75
Arg Ser Leu Tyr	Asn Gly Leu Val Ala	Gly Leu Gln Arg Gln	Met
80		85	90
Ser Phe Ala Ser	Val Arg Ile Gly Leu	Tyr Asp Ser Val Lys	Gln
95		100	105

Phe Tyr Thr Lys Gly Ser Glu His Ala Ser Ile Gly Ser Arg Leu	110	115	120
Leu Ala Gly Ser Thr Thr Gly Ala Leu Ala Val Ala Val Ala Gln	125	130	135
Pro Thr Asp Val Val Lys Val Arg Phe Gln Ala Gln Ala Arg Ala	140	145	150
Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val Asn Ala Tyr Lys Thr	155	160	165
Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp Lys Gly Thr Ser	170	175	180
Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala Glu Leu Val	185	190	195
Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn Leu Met	200	205	210
Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala Gly	215	220	225
Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr	230	235	240
Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His	245	250	255
Cys Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr	260	265	270
Lys Gly Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val	275	280	285
Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala	290	295	300
Ala Cys Thr Ser Arg Glu Ala Pro Phe	305		

<210> 18
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Ala Val Lys Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala
 1 5 10 15
 Asp Leu Val Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln
 20 25 30
 Ile Gln Gly Glu Asn Gln Ala Val Gln Thr Ala Arg Leu Val Gln
 35 40 45

Tyr Arg Gly Val	Leu Gly Thr Ile Leu Thr Met Val Arg Thr Glu	50	55	60
Gly Pro Cys Ser	Pro Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg	65	70	75
Gln Met Ser Phe	Ala Ser Ile Arg Ile Gly Leu Tyr Asp Ser Val	80	85	90
Lys Gln Val Tyr	Thr Pro Lys Gly Ala Asp Asn Ser Ser Leu Thr	95	100	105
Thr Arg Ile Leu	Ala Gly Cys Thr Thr Gly Ala Met Ala Val Thr	110	115	120
Cys Ala Gln Pro	Thr Asp Val Val Lys Val Arg Phe Gln Ala Ser	125	130	135
Ile His Leu Gly	Pro Ser Arg Ser Asp Arg Lys Tyr Ser Gly Thr	140	145	150
Met Asp Ala Tyr	Arg Thr Ile Ala Arg Glu Glu Gly Val Arg Gly	155	160	165
Leu Trp Lys Gly	Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val	170	175	180
Asn Cys Ala Glu	Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu	185	190	195
Leu Asp Tyr His	Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val	200	205	210
Ser Ala Phe Gly	Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro	215	220	225
Val Asp Val Val	Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln	230	235	240
Tyr Phe Ser Pro	Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu	245	250	255
Gly Pro Thr Ala	Phe Tyr Lys Gly Phe Thr Pro Ser Phe Leu Arg	260	265	270
Leu Gly Ser Trp	Asn Val Val Met Phe Val Thr Tyr Glu Gln Leu	275	280	285
Lys Arg Ala Leu	Met Lys Val Gln Met Leu Arg Glu Ser Pro Phe	290	295	300
